



SEQUENCE LISTING

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OKI, HIROYUKI
YAMAGUCHI, HIROTAKA

<120> METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND
GENE THEREOF

<130> 55022-DIV (71526)

<140> 10/625,821
<141> 2003-07-22

<150> 09/646,825
<151> 2000-09-22

<150> JP/10-96637
<151> 1998-03-24

<160> 38

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic
saccharomyces cerevisiae

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<222> (20)..(2077)

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Ile Ser Phe Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
15 20 25

tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag 148
Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
30 35 40

tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act 196
Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
45 50 55

gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct 244
Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
60 65 70 75

ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg	292
Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu	
80 85 90	
gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct	340
Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala	
95 100 105	
cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca	388
Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala	
110 115 120	
aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac	436
Asn Glu Thr Ala Tyr His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His	
125 130 135	
ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc	484
Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe	
140 145 150 155	
tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc	532
Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg	
160 165 170	
gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc	580
Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile	
175 180 185	
tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg	628
Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp	
190 195 200	
aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt	676
Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val	
205 210 215	
ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac	724
Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn	
220 225 230 235	
atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg	772
Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met	
240 245 250	
gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc	820
Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro	
255 260 265	
gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc	868
Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr	
270 275 280	
gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac	916
Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr	
285 290 295	

gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca	964
Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser	
300 305 310 315	
gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc	1012
Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe	
320 325 330	
aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag	1060
Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Phe Gln	
335 340 345	
tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att	1108
Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile	
350 355 360	
cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc	1156
His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys	
365 370 375	
cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc	1204
His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu	
380 385 390 395	
tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt	1252
Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly	
400 405 410	
ctt aag acc gcc act ttg tgc acc aca gat gat tct aac gtt atc aag	1300
Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys	
415 420 425	
atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt	1348
Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe	
430 435 440	
gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt	1396
Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe	
445 450 455	
caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac	1444
Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn	
460 465 470 475	
aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg	1492
Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr	
480 485 490	
aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat	1540
Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp	
495 500 505	
tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att	1588
Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile	
510 515 520	

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gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg 1636
Ala Lys Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val
525 530 535

gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act 1684
Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr
540 545 550 555

gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac 1732
Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His
560 565 570

ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt 1780
Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys
575 580 585

gaa gtc tct gtc atc tac act ggg tca tca gtg gag gat aca aac tca 1828
Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser
590 595 600

gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc 1876
Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr
605 610 615

gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca 1924
Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser
620 625 630 635

gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca 1972
Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser
640 645 650

tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa 2020
Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln
655 660 665

ggg atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt 2068
Gly Ile Asp Ser Ser Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser
670 675 680

ttt act tgg taagagctca agctt 2092
Phe Thr Trp
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<210> 2
<211> 686
<212> PRT
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<220>
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      saccharomyces cerevisiae

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Ala	Ala	Leu	Tyr	Gln	Phe	Gly	Cys	Ser	Ser	Lys	Ser	Lys	Ser	Cys	Tyr	35	40	45
Cys	Lys	Asn	Ile	Asn	Trp	Leu	Gly	Ser	Val	Thr	Ala	Cys	Ala	Tyr	Glu	50	55	60
Asn	Ser	Lys	Ser	Asn	Lys	Thr	Leu	Asp	Ser	Ala	Leu	Met	Lys	Leu	Ala	65	70	75
Ser	Gln	Cys	Ser	Ser	Ile	Lys	Val	Tyr	Thr	Leu	Glu	Asp	Met	Lys	Asn	85	90	95
Ile	Tyr	Leu	Asn	Ala	Ser	Asn	Tyr	Leu	Arg	Ala	Pro	Glu	Lys	Ser	Asp	100	105	110
Lys	Lys	Thr	Val	Val	Ser	Gln	Pro	Leu	Met	Ala	Asn	Glu	Thr	Ala	Tyr	115	120	125
His	Tyr	Tyr	Tyr	Glu	Glu	Asn	Tyr	Gly	Ile	His	Leu	Asn	Leu	Met	Arg	130	135	140
Ser	Gln	Trp	Cys	Ala	Trp	Gly	Leu	Val	Phe	Phe	Trp	Val	Ala	Val	Leu	145	150	155
Thr	Ala	Ala	Thr	Ile	Leu	Asn	Ile	Leu	Lys	Arg	Val	Phe	Gly	Lys	Asn	165	170	175
Ile	Met	Ala	Asn	Ser	Val	Lys	Lys	Ser	Leu	Ile	Tyr	Pro	Ser	Val	Tyr	180	185	190
Lys	Asp	Tyr	Asn	Glu	Arg	Thr	Phe	Tyr	Leu	Trp	Lys	Arg	Leu	Pro	Phe	195	200	205
Asn	Phe	Thr	Thr	Arg	Gly	Lys	Gly	Leu	Val	Val	Leu	Ile	Phe	Val	Ile	210	215	220
Leu	Thr	Ile	Leu	Ser	Leu	Ser	Phe	Gly	His	Asn	Ile	Lys	Leu	Pro	His	225	230	235
Pro	Tyr	Asp	Arg	Pro	Arg	Trp	Arg	Arg	Ser	Met	Ala	Phe	Val	Ser	Arg	245	250	255
Arg	Ala	Asp	Leu	Met	Ala	Ile	Ala	Leu	Phe	Pro	Val	Val	Tyr	Leu	Phe	260	265	270
Gly	Ile	Arg	Asn	Asn	Pro	Phe	Ile	Pro	Ile	Thr	Gly	Leu	Ser	Phe	Ser	275	280	285
Thr	Phe	Asn	Phe	Tyr	His	Lys	Trp	Ser	Ala	Tyr	Val	Cys	Phe	Met	Leu	290	295	300
Ala	Val	Val	His	Ser	Ile	Val	Met	Thr	Ala	Ser	Gly	Val	Lys	Arg	Gly	305	310	315
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Val	Phe	Gln	Ser	Leu	Val	Arg	Lys	Phe	Tyr	Phe	Arg	Trp	Gly	Ile	Val	325	330	335	
Ala	Thr	Ile	Leu	Met	Ser	Ile	Ile	Ile	Phe	Gln	Ser	Glu	Lys	Val	Phe	340	345	350	
Arg	Asn	Arg	Gly	Tyr	Glu	Ile	Phe	Leu	Leu	Ile	His	Lys	Ala	Met	Asn	355	360	365	
Ile	Met	Phe	Ile	Ile	Ala	Met	Tyr	Tyr	His	Cys	His	Thr	Leu	Gly	Trp	370	375	380	
Met	Gly	Trp	Ile	Trp	Ser	Met	Ala	Gly	Ile	Leu	Cys	Phe	Asp	Arg	Phe	385	390	395	400
Cys	Arg	Ile	Val	Arg	Ile	Ile	Met	Asn	Gly	Gly	Leu	Lys	Thr	Ala	Thr	405	410	415	
Leu	Ser	Thr	Thr	Asp	Asp	Ser	Asn	Val	Ile	Lys	Ile	Ser	Val	Lys	Lys	420	425	430	
Pro	Lys	Phe	Phe	Lys	Tyr	Gln	Val	Gly	Ala	Phe	Ala	Tyr	Met	Tyr	Phe	435	440	445	
Leu	Ser	Pro	Lys	Ser	Ala	Trp	Phe	Tyr	Ser	Phe	Gln	Ser	His	Pro	Phe	450	455	460	
Thr	Val	Leu	Ser	Glu	Arg	His	Arg	Asp	Pro	Asn	Asn	Pro	Asp	Gln	Leu	465	470	475	480
Thr	Met	Tyr	Val	Lys	Ala	Asn	Lys	Gly	Ile	Thr	Arg	Val	Leu	Leu	Ser	485	490	495	
Lys	Val	Leu	Ser	Ala	Pro	Asn	His	Thr	Val	Asp	Cys	Lys	Ile	Phe	Leu	500	505	510	
Glu	Gly	Pro	Tyr	Gly	Val	Thr	Val	Pro	His	Ile	Ala	Lys	Leu	Lys	Arg	515	520	525	
Asn	Leu	Val	Gly	Val	Ala	Ala	Gly	Leu	Gly	Val	Ala	Ala	Ile	Tyr	Pro	530	535	540	
His	Phe	Val	Glu	Cys	Leu	Arg	Leu	Pro	Ser	Thr	Asp	Gln	Leu	Gln	His	545	550	555	560
Lys	Phe	Tyr	Trp	Ile	Val	Asn	Asp	Leu	Ser	His	Leu	Lys	Trp	Phe	Glu	565	570	575	
Asn	Glu	Leu	Gln	Trp	Leu	Lys	Glu	Lys	Ser	Cys	Glu	Val	Ser	Val	Ile	580	585	590	
Tyr	Thr	Gly	Ser	Ser	Val	Glu	Asp	Thr	Asn	Ser	Asp	Glu	Ser	Thr	Lys	595	600	605	
Gly	Phe	Asp	Asp	Lys	Glu	Glu	Ser	Glu	Ile	Thr	Val	Glu	Cys	Leu	Asn	610	615	620	

Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
625 630 635 640

Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr
645 650 655

Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser
660 665 670

Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser Phe Thr Trp
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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<400> 4
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<210> 5
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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cttcgctaca gtccaatcga gcg                                     83
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<210> 6
<211> 83
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

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 ttcggatgct caagcaagtc aaa 83

<210> 7
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 gcgcttatga gaactccaaa tct 83

<210> 8
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
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 agagtcttgt tagatttgga gtt 83

<210> 9
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
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<210> 10
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 gtgaaacaac tgtcttctta tcg 83

<210> 11

<211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 12
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 13
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 14
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer

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 taaagttgaa tggcaaactg 80

<210> 15
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer

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ccgaaagaga gtgagagaat 80

<210> 16
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 17
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 18
<211> 83
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<211> 83
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<220>
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<210> 20
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<220>
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<210> 21
<211> 83
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 22
<211> 83
<212> DNA
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<220>
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<210> 24
<211> 82
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<220>

<223> Description of Artificial Sequence: Primer

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<210> 25

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 26

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 27

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 28

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

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 gagctacaat ggcttaa 77

<210> 30
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 <212> DNA
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<220>
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<210> 31
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 aatgccttaa caagagg 77

<210> 32
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 <213> Artificial Sequence

<220>
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<211> 77

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<223> Description of Artificial Sequence: Primer

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<210> 35

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

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<210> 36

<211> 2059

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 36

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 tgtgcctatg agaattccaa atctaacaaa aactagaca gcgccttaat gaagttagca 240
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 gcgtaaaatt atttgagagc acctgagaaa agtgataaaa aaaccgtggt tagtcaaccg 360
 ctcatggcga acgagacagc gtatcattat tattatgagg aaaattatgg tatccatctt 420
 aacctaatgc gctctcaatg gtgcgcttg ggctcgtct tcttctgggt ggggtgtgctt 480
 actgcagcca ctatcttgaa cattctgaaa aggggtgttg gtaagaacat catggcaaac 540
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 atgtctatta ttattttcca aagtgaaaaa gtatttagaa atagagggtg tgagatattc 1080
 cttcttattc ataaagcgat gaattattatg ttcattattg ccatgtacta ccattgtcac 1140

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<210> 37
<211> 180
<212> DNA
<213> Saccharomyces cerevisiae

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<220>
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gaa cga act ttt tat tta tgg aag cgt cta cca ttt aat ttt aca act 96
Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
20 25 30

cga ggc aag ggt ctc gtc gta tta att ttt gtt att ttg act ata tta 144
Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
35 40 45

tct ctc agt ttt ggt cat aat att aaa ctt cca cac 180
Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
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<210> 38
<211> 60
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 38
Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr Lys Asp Tyr Asn
1 5 10 15

Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
20 25 30

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Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
35 40 45

Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
50 55 60